



[illegible]

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gi3746533_human	194	SLALMAHTILFLKLF	SYRDVNSWCR--RARAKAASAGKKASSAAAPHTVSYPDNLT
SEQ25_mouse	203	SVFALASYSIMFLKLY	SYRDVNLWCRQRRVKAKAVSTGKKVSGAAQAVSYPDNLT
SEQ26_Arab	239	VTLMLLT-CIVWLKLV	SYAHTSY--DIRSLANAADKANP-----EVSYYV--SLKS
SEQ2_Arab	239	VTLMLLT-CIVWLKLV	SYAHTSY--DIRSLANAADKANP-----EVSYYV--SLKS
SEQ14_rice	211	FLLFIA-CIVWLKLV	FAHTNH--DIRQLTMGGKKVDNELSTVMDNQLQPP---TLGN
SEQ16_soy	215	VTLMIFS-CVVWLKLV	SYAHTNY--DMRALTKLVEKGEALLDTLNMDPYINV--SFKS
SEQ22_wheat	218	FVLMFIA-SITWLKLV	FAHTNY--DIRILSQSIEKGATHGSSIDEENIKGP---TINS
	241		

[illegible]

gi3746533_human	312	KDMDYSRIIERLLKLVAPNHLIWLIFFFYWLFSCLNAVAELMQFGDREFYRDWWNSESVT	
SEQ25_mouse	323	KDMDYSRIIERLLKLVAPNHLIWLIFFFYWFHSCLNVAEELLQFGDREFYRDWWNAESVT	
SEQ26_Arab	345	KG-DLLYAIERVLKLSVPNLVWLCMFYCFFFHLWLNLIAELLCFGDREFYKDWWNAKSVG	
SEQ2_Arab	345	KG-DLLYAIERVLKLSVPNLVWLCMFYCFFFHLWLNLIAELLCFGDREFYKDWWNAKSVG	
SEQ14_rice	324	KG-GLLNAVETVLKLSLPNVYLWLCMFYAFFHLWLSILAEILRFGDREFYKDWWNAKTID	
SEQ16_soy	328	KG-NLLYATERVLKLSVPNLVWLCMFYCFFFHLWLNLIAELLRFGDREFYKDWWNAKTVE	
SEQ22_wheat	331	NG-NFLDAIERVLKLSVPTLVWLCMFYSFFHLWLNLIAELLRFGDREFYKDWWNAKTVE	
	361		
		FYXDWWN	420
		Domain-A	

[illegible]

# APPENDIX Id

gi3746533_human	432	TGMMAQIPLAWFVGRFFQGNYGNAAV-----WLSL-IGQPIAVLMYVHDYYVVLNYEAPA	*	*	*	*	*	*	*	*
SEQ25_mouse	443	TAMMAQVPLAWIVGRFFQGNYGNAAV-----WVTL-IGQPVALMYVHDYYVVLNYDAPV	*	*	*	*	*	*	*	*
SEQ26_Arab	464	LGIMFQVPLV-FITNYLQERF-GSTVGNMIFWFIFCI FGQPMC VLLY----YHDL MNRKGS	*	*	*	*	*	*	*	*
SEQ2_Arab	464	LGIMFQVPLV-FITNYLQERF-GSTVGNMIFWFIFCI FGQPMC VLLY----YHDL MNRKGS	*	*	*	*	*	*	*	*
SEQ14_rice	443	LGIMLQIPLI-VLTAYLKSKFRDTMVGNMIFWFFFCIYGQPMC LLLY----YHDVMNR IEK	*	*	*	*	*	*	*	*
SEQ16_soy	447	GGIMFQVPLV-LITNYLQNKFRNSMVGNMIFWFIFSI LGQPMC VLLY----YHDL MNRK GK	*	*	*	*	*	*	*	*
SEQ22_wheat	450	SGIMFQIPLL-FLTKYLQDKFKNTMVGNMIFWFFFSI VGQPMC VLLY----YHDVMNRQAQ	*	*	*	*	*	*	*	*
	481									

gi3746533_human	486	AEA	488
SEQ25_mouse	497	G-V	498
SEQ26_Arab	519	MS-	520
SEQ2_Arab	519	MS-	520
SEQ14_rice	499	AR-	500
SEQ16_soy	503	LD-	504
SEQ22_wheat	506	TNG	508
			541